

Resource Summary Report

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Peroxisome Database

RRID:SCR_008352

Type: Tool

Proper Citation

Peroxisome Database (RRID:SCR_008352)

Resource Information

URL: <http://www.peroxisomedb.org/>

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Description: The aim of the PEROXISOME database (PeroxisomeDB) is to gather, organize and integrate curated information on peroxisomal genes, their encoded proteins, their molecular function and metabolic pathway they belong to, and their related disorders. PeroxisomeDB contains the complete peroxisomal proteome of Homo sapiens (encoded by 85 genes) and Saccharomyces cerevisiae (encoded by 61 genes). Now, we have included 34 new organism genomes with the acquisition of 2426 new peroxisomal homolog proteins. PeroxisomeDB 2.0 integrates the peroxisomal metabolome of whole microbody family by the new incorporation of the glycosome proteomes of trypanosomatids and the glyoxysome proteome of Arabidopsis thaliana. The site also provides a Peroxisome Metabolome of peroxisomal genes and proteins, their molecular interactions and metabolic pathways, tools for comparative genomics, predictive tools. Sponsors: Peroxisome Database is funded by Institut de Gntique et deBiologie Molculaire et Cellulaire.

Synonyms: Preoisomedb

Resource Type: data or information resource, database

Keywords: family, function, gene, arabidopsis thaliana, disorder, genome, genomic, glycosome, glyoxysome, homolog, homo sapiens, interaction, metabolic, metabolome, microbody, molecular, organism, pathway, peroxisome, protein, proteome, saccharomyces cerevisiae, trypanosomatid

Resource Name: Peroxisome Database

Resource ID: SCR_008352

Alternate IDs: nif-0000-25216

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260801T190956+0000

Ratings and Alerts

No rating or validation information has been found for Peroxisome Database.

No alerts have been found for Peroxisome Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Hunt LC, et al. (2023) An adaptive stress response that confers cellular resilience to decreased ubiquitination. *Nature communications*, 14(1), 7348.

Villalba GC, et al. (2021) Fantastic databases and where to find them: Web applications for researchers in a rush. *Genetics and molecular biology*, 44(2), e20200203.

Liang Z, et al. (2021) Newly identified genes contribute to vanillin tolerance in *Saccharomyces cerevisiae*. *Microbial biotechnology*, 14(2), 503.

Verner Z, et al. (2021) Anaerobic peroxisomes in *Entamoeba histolytica* metabolize myo-inositol. *PLoS pathogens*, 17(11), e1010041.

Anteghini M, et al. (2021) In-Pero: Exploiting Deep Learning Embeddings of Protein Sequences to Predict the Localisation of Peroxisomal Proteins. *International journal of molecular sciences*, 22(12).

Coppa A, et al. (2020) The peroxisomal fatty acid transporter ABCD1/PMP-4 is required in the *C. elegans* hypodermis for axonal maintenance: A worm model for adrenoleukodystrophy. *Free radical biology & medicine*, 152, 797.

Rusilowicz-Jones EV, et al. (2020) USP30 sets a trigger threshold for PINK1-PARKIN amplification of mitochondrial ubiquitylation. *Life science alliance*, 3(8).

Kunze M, et al. (2020) The type-2 peroxisomal targeting signal. *Biochimica et biophysica acta. Molecular cell research*, 1867(2), 118609.

Van Dolah FM, et al. (2020) Transcriptomic analysis of polyketide synthases in a highly ciguatoxic dinoflagellate, *Gambierdiscus polynesiensis* and low toxicity *Gambierdiscus pacificus*, from French Polynesia. *PloS one*, 15(4), e0231400.

Song J, et al. (2018) Dysregulation of the NUDT7-PGAM1 axis is responsible for chondrocyte death during osteoarthritis pathogenesis. *Nature communications*, 9(1), 3427.

Launay N, et al. (2017) Tauroursodeoxycholic bile acid arrests axonal degeneration by inhibiting the unfolded protein response in X-linked adrenoleukodystrophy. *Acta neuropathologica*, 133(2), 283.

Ámon J, et al. (2017) A eukaryotic nicotinate-inducible gene cluster: convergent evolution in fungi and bacteria. *Open biology*, 7(12).

Haimovich G, et al. (2016) A role for mRNA trafficking and localized translation in peroxisome biogenesis and function? *Biochimica et biophysica acta*, 1863(5), 911.

Reumann S, et al. (2016) Characterization, prediction and evolution of plant peroxisomal targeting signals type 1 (PTS1s). *Biochimica et biophysica acta*, 1863(5), 790.

Yaegashi J, et al. (2015) Genome mining and molecular characterization of the biosynthetic gene cluster of a diterpenic meroterpenoid, 15-deoxyoxalicine B, in *Penicillium canescens*. *Chemical science*, 6(11), 6537.

Fourcade S, et al. (2015) Oxidative stress, mitochondrial and proteostasis malfunction in adrenoleukodystrophy: A paradigm for axonal degeneration. *Free radical biology & medicine*, 88(Pt A), 18.

Gawryluk RM, et al. (2014) Compositional complexity of the mitochondrial proteome of a unicellular eukaryote (*Acanthamoeba castellanii*, supergroup Amoebozoa) rivals that of animals, fungi, and plants. *Journal of proteomics*, 109, 400.

Lam C, et al. (2014) Two novel compound heterozygous mutations in OPA3 in two siblings with OPA3-related 3-methylglutaconic aciduria. *Molecular genetics and metabolism reports*, 1, 114.

Lodhi IJ, et al. (2014) Peroxisomes: a nexus for lipid metabolism and cellular signaling. *Cell metabolism*, 19(3), 380.

Stiebler AC, et al. (2014) Ribosomal readthrough at a short UGA stop codon context triggers dual localization of metabolic enzymes in Fungi and animals. *PLoS genetics*, 10(10), e1004685.